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MParch_pp protein - protein database search, using Smith-Waterman algorithm
F0000n: Wed Aug 16 09:45:05 2000; Maspar time 5.58 Seconds
560.903 Million cell updates/sec
Tabular output not generated.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Rank	Score	Query Match	Length	DB ID	Description	Pred. No.
1	664	97.2	101	1	CVN_NOSEL	3.44e-138
2	103	15.1	327	1	ACCO_DORSP	3.79e-04
3	92	13.5	416	1	RHLA_PANTR	2.79e-02
4	91	13.3	416	1	RHD_HUMAN	4.06e-02
5	91	13.3	505	1	ACHB_BOVIN	4.06e-02
6	90	13.2	416	1	RHL_MACMU	5.89e-02
7	89	13.0	416	1	RHLR_PANTR	8.54e-02
8	86	12.6	353	1	RHL_HLYPI	2.55e-01
9	86	12.6	392	1	VATC_YEAST	2.55e-01
10	86	12.6	1014	1	NANH_CLOSE	2.55e-01
11	85	12.4	223	1	AOP2_MOUSE	3.65e-01
12	85	12.4	223	1	AOP2_HUMAN	3.65e-01
13	85	12.4	501	1	ACHB_RAT	3.65e-01
14	85	12.4	501	1	ACHB_HUMAN	3.65e-01
15	85	12.4	501	1	ACHB_MOUSE	3.65e-01
16	84	12.3	223	1	AOX2_RAT	5.21e-01
17	83	12.2	223	1	AOP2_BOVIN	7.42e-01
18	83	12.2	416	1	RHLD_GORGO	7.42e-01
19	82	12.0	717	1	CLAI_ARATH	1.05e+00
20	81	11.9	320	1	ACC3_CUCME	1.49e+00
21	81	11.9	419	1	HFLK_ECOLI	1.49e+00
22	81	11.9	683	1	VTER_HSVSA	1.49e+00
23	80	11.7	450	1	ENV2_ECOLI	2.10e+00

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RT relationship with the R-C-E-F blood group system, the chimpanzee
RT counterpart of the human rhesus system."
RL Biochem. Genet. 32:201-221(1994).
CC -!- FUNCTION: MAY BE PART OF AN OLIGOMERIC COMPLEX WHICH IS LIKELY TO
CC HAVE A TRANSPORT OR CHANNEL FUNCTION IN THE ERYTHROCYTE MEMBRANE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE RH FAMILY.
CC -----
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CC -----
CC EMBL: L37049; AAA65623.1;
CC PFM: PF00909; Ammonium transp; 1.
CC PRINTS: PR00342; RHESUSRHD.
CC Erythrocyte; Transmembrane.
CC INIT_MET 0 0
CC FT TRANSMEM 11 31 BY SIMILARITY.
CC FT TRANSMEM 43 63 POTENTIAL.
CC FT TRANSMEM 76 96 POTENTIAL.
CC FT TRANSMEM 124 144 POTENTIAL.
CC FT TRANSMEM 171 191 POTENTIAL.
CC FT TRANSMEM 202 222 POTENTIAL.
CC FT TRANSMEM 237 257 POTENTIAL.
CC FT TRANSMEM 264 284 POTENTIAL.
CC FT TRANSMEM 286 306 POTENTIAL.
CC FT TRANSMEM 330 350 POTENTIAL.
CC FT TRANSMEM 357 377 POTENTIAL.
CC SQ SEQUENCE 416 AA; 45461 MW; B0B566734DB5E14D CRC64;

Query Match 13.5%; Score 92; DB 1; Length 416;
Best Local Similarity 23.7%; Pred. No. 2.79e-02;
Matches 22; Conservative 30; Mismatches 36; Indels 5; Gaps 5;

Db 220 PSFNSALLRSPERKNAFTYAVAV-SVVTASGSLAHPOGKISMSYMNVLAVGV 278
QY 11 SAIGSVLTSTCETNGYNTS-SIDLNSVENVGDS-LKQPSNFICT-RNTQLAGSS 67
Db 279 AVGTSCHLITSPWLAVLGLVAGLISIGA-KY 310
QY 68 ELAECETRAQOFVSTKINLDDHIANIDGLTKY 100

RESULT 4
ID RHD_HUMAN STANDARD; PRT: 416 AA.
AC Q02161; Q02162; Q07618; Q16355; Q16147; Q16235;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE BLOOD GROUP RH(D) POLYPEPTIDE (RHESUS D ANTIGEN) (RHIII) (RH
DE POLYPEPTIDE 2) (RHPII).
GN RHD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=BONE MARROW;
RC MEDLINE; 93086356.
RA le van Kim C., Mouro I., Cherif-Zahar B., Raynal V., Cherrier C.,
RA Carttron J.-P., Colin Y.;
RT "Molecular cloning and primary structure of the human blood group Rhd
RT polypeptide."
RL Proc. Natl. Acad. Sci. U.S.A. 89:10925-10929(1992).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=BONE MARROW;
RC MEDLINE; 92360855.
RA le van Kim C., Cherif-Zahar B., Raynal V., Mouro I., Lopez M.,
```

RA Cartton J.-P., Colin Y.;
 RT "Multiple Rh messenger RNA isoforms are produced by alternative
 RL splicing."; Blood 80:1074-1078(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 93320449.
 RA Lucie M.A., Thompson E.S., Wagner S., Coyne K.E., Ferdman B.A.,
 RL Lublin D.M.;
 RT "Molecular cloning of RHD cDNA derived from a gene present in RHD-
 RL positive, but not Rhd-negative individuals."; Blood 82:651-655(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 93216282.
 RA Kajii E., Umenishi F., Iwamoto S., Ikemoto S.;
 RT "Isolation of a new cDNA clone encoding an Rh polypeptide associated
 RL with the Rh blood group system."; Hum. Genet. 91:157-162(1993).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 95329738.
 RA Huang C.H., Reid M.E., Chen Y.;
 RT "Identification of a partial internal deletion in the RH locus
 RL causing the human erythrocyte D-phenotype."; Blood 86:784-790(1995).
 RN [6]
 RP SEQUENCE FROM N.A. (SHORT FORM 1).
 RX MEDLINE: 94235883.
 RA Westhoff C.M., Wylie D.E.;
 RT "Identification of a new Rhd-specific mRNA from K562 cells."; Blood 83:3098-3100(1994).
 RN [7]
 RP SEQUENCE FROM N.A. (SHORT FORM 2).
 RX MEDLINE: 94362249.
 RA Suyana K., Lunn R., Haller S., Goldstein J.;
 RT "Rh(D) antigen expression and isolation of a new Rh(D) cDNA isoform
 RL in human erythroleukemic K562 cells."; Blood 84:1975-1981(1994).
 RN [8]
 RP VARIANT BLOOD GROUP TAR.
 RX MEDLINE: 95259709.
 RA Rouillac C., Le van Kim C., Beolet M., Cartton J.-P., Colin Y.;
 RT "Leu10Pro substitution in the Rhd polypeptide is responsible for the
 RL Dvii category blood group phenotype."; Am. J. Hematol. 49:87-88(1995).
 CC -!- FUNCTION: MAY BE PART OF AN OLIGOMERIC COMPLEX WHICH IS LIKELY TO
 CC HAVE A TRANSPORT OR CHANNEL FUNCTION IN THE ERYTHROCYTE MEMBRANE.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- ALTERNATIVE PRODUCTS: VARIOUS FORMS ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -!- TISSUE SPECIFICITY: RESTRICTED TO TISSUES OR CELL LINES EXPRESSING
 CC ERYTHROID CHARACTERS.
 CC -!- POLYMORPHISM: RHD AND RHCE ARE RESPONSIBLE FOR THE RH BLOOD GROUP
 CC SYSTEM. THE MOLECULAR BASIS OF THE TAR-RH40 BLOOD GROUP ANTIGEN
 CC IS A POLYMORPHISM IN POSITION 109.
 CC -!- SIMILARITY: BELONGS TO THE RH FAMILY. STRONG, TO RHCE.
 CC
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 CC
 CC EMBL: X63097; CAA44811.1;
 CC EMBL: X63094; CAA44808.1;
 CC EMBL: L08429; AAA02679.1;
 CC EMBL: S57971; AAB26081.1;
 CC EMBL: S78509; AAB34852.1;
 CC EMBL: S70174; AAB30756.1;
 CC EMBL: S73913; AAB31911.1;

DR PIR: S26564; S26564.
 DR MIM: I11680; -.
 DR PFRM: PF00909; Ammonium_transp; 1.
 DR PRINTS: PR00342; RHESUSRHD.
 KW Erythrocyte; Transmembrane; Blood group antigen; Alternative splicing;
 RN Polymorphism.
 FT INIT_MET 0 0
 FT TRANSMEM 11 31 POTENTIAL.
 FT TRANSMEM 43 63 POTENTIAL.
 FT TRANSMEM 76 96 POTENTIAL.
 FT TRANSMEM 106 126 POTENTIAL.
 FT TRANSMEM 129 149 POTENTIAL.
 FT TRANSMEM 166 186 POTENTIAL.
 FT TRANSMEM 202 222 POTENTIAL.
 FT TRANSMEM 237 257 POTENTIAL.
 FT TRANSMEM 286 306 POTENTIAL.
 FT TRANSMEM 333 353 POTENTIAL.
 FT TRANSMEM 357 377 POTENTIAL.
 FT VARSPLIC 313 408 MISSING (IN SHORT ISOFORM 1).
 FT VARSPLIC 315 415 C -> S (IN SHORT ISOFORM 2).
 FT VARSPLIC 316 416 MISSING (IN SHORT ISOFORM 2).
 FT VARIANT 109 109 L -> P (IN TAR ANTIGEN).
 FT VARIANT 217 217 M -> I.
 FT VARIANT 217 217 /FTID-VAR_006920.
 FT CONFLICT 15 15 W -> C (IN REF. 5).
 FT CONFLICT 38 38 E -> G (IN REF. 4).
 FT CONFLICT 102 102 S -> P (IN REF. 4).
 FT CONFLICT 126 126 V -> A (IN REF. 4).
 FT CONFLICT 173 173 V -> M (IN REF. 5).
 FT CONFLICT 181 181 S -> T (IN REF. 4).
 FT CONFLICT 313 313 G -> V (IN REF. 4 AND 7).
 FT CONFLICT 322 322 P -> H (IN REF. 4).
 FT CONFLICT 397 397 E -> V (IN REF. 5).
 SQ SEQUENCE 416 AA; 45049 MW; 9136DF1A37D76B1B CRC64;
 Query Match 13.3%; Score 91; DB 1; Length 416;
 Best Local Similarity 22.6%; Pred. No. 4,06e-02;
 Matches 21; Conservative 31; Mismatches 36; Indels 5; Gaps 5;
 Db 220 PSFNSALLRSPTEKNAVENTYVAVAV-SVVTATSGSSLAHPQKISKTYVHSAVLGGV 278
 QY 11 SAIQGVLSTCETRTNGGNTS-SIDLSNVIEVDGS-LKWQSPNFIETC-RNTQLAGSS 67
 Db 279 AVGTCSHLIPSPWLAIVGLVAGLSVGGG-KY 310
 QY 68 ELAAECKTRAQQFVSTKINDDHIANIDGLTKY 100
 RESULT 5
 ID ACHE_BOVIN STANDARD; PRT; 505 AA.
 AC P04758;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE ACETYLCHOLINE RECEPTOR PROTEIN, BETA CHAIN PRECURSOR.
 GN CHRNBL.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 85003649.
 RA Tanabe T., Noda M., Furutani Y., Takai T., Takahashi H., Tanaka K.,
 RA Hirose T., Inayama S., Numa S.;
 RT "Primary structure of beta subunit precursor of calf muscle
 RL acetylcholine receptor deduced from cDNA sequence."; Eur. J. Biochem. 144:11-17(1984).
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.

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CC EMBL: L37050; AAA65624.1; -

CC PFAM: PF00909; Ammonium transp; 1.

CC PRINTS: PR00342; RHESUSRD.

CC Erythrocyte; Transmembrane.

CC INIT_MET 0 0 BY SIMILARITY.

CC FT TRANS MEM 11 31 POTENTIAL.

CC FT TRANS MEM 43 63 POTENTIAL.

CC FT TRANS MEM 76 96 POTENTIAL.

CC FT TRANS MEM 124 144 POTENTIAL.

CC FT TRANS MEM 171 191 POTENTIAL.

CC FT TRANS MEM 202 222 POTENTIAL.

CC FT TRANS MEM 237 257 POTENTIAL.

CC FT TRANS MEM 264 284 POTENTIAL.

CC FT TRANS MEM 286 306 POTENTIAL.

CC FT TRANS MEM 330 350 POTENTIAL.

CC FT TRANS MEM 357 377 POTENTIAL.

CC SEQUENCE 416 AA; 45299 MW; C05SD7CC8B4A0420 CRC64;

Query Match 13.0%; Score 89; DB 1; Length 416;

Best Local Similarity 22.6%; Pred. No. 8.54e-02;

Matches 21; Conservative 31; Mismatches 36; Indels 5; Gaps 5;

Db 220 PSNSALLRPIERKNVFNYYAV-SVVTAGSSSLAHPOCKISMSYMHNAVLGGV 278

QY 11 SAIGSVLTSTCERTNGYNTS-SIDLNSVIENVGDS-LKWQPSNFIETC-RNTQLAGSS 67

Db 279 AVGTSCHLSPWLMVGLVGLISVGGA-KY 310

QY 68 ELAECKTRAQFVSTKINLDDHIANIDGTLY 100

RESULT 8
ID RHL_HYLP1 STANDARD; PRT; 353 AA.

AC Q28446; 1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE RH-LIKE PROTEIN (RHESUS-LIKE PROTEIN).

OS Hylobates pileatus (Pileated gibbon).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BONE MARROW;

RA MEDLINE; 95085595.

RA Salvioli I., Blancher A., Calvas P., Clayton J., Socha W.W.,

RA Colin Y., Ruffie J.;

RT "Molecular genetics of chimpanzee Rh-related genes: their

RT relationship with the R-C-E-F blood group system, the chimpanzee

RT counterpart of the human rhesus system.";

RT Biochem. Genet. 32:201-221(1994).

CC -!- FUNCTION: MAY BE PART OF AN OLIGOMERIC COMPLEX WHICH IS LIKELY TO

CC HAVE A TRANSPORT OR CHANNEL FUNCTION IN THE ERYTHROCYTE MEMBRANE.

CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -!- SIMILARITY: BELONGS TO THE RH FAMILY.

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CC EMBL: L37051; AAA65625.1; -

CC PFAM: PF00909; Ammonium transp; 1.

CC Erythrocyte; Transmembrane.

CC INIT_MET 0 0 BY SIMILARITY.

CC FT TRANS MEM 10 30 POTENTIAL.

CC FT TRANS MEM 44 64 POTENTIAL.

FT TRANS MEM 76 96 POTENTIAL.

FT TRANS MEM 124 144 POTENTIAL.

FT TRANS MEM 166 186 POTENTIAL.

FT TRANS MEM 208 228 POTENTIAL.

FT TRANS MEM 237 257 POTENTIAL.

FT TRANS MEM 286 306 POTENTIAL.

FT TRANS MEM 353 AA; 38417 MW; 3CFD25B38033AB6A CRC64;

QY SEQUENCE 353 AA; 38417 MW; 3CFD25B38033AB6A CRC64;

Query Match 12.6%; Score 86; DB 1; Length 353;

Best Local Similarity 21.3%; Pred. No. 2.55e-01;

Matches 19; Conservative 31; Mismatches 37; Indels 2; Gaps 2;

Db 220 PSNSALLRPIERKNVFNYYAV-SVVTAGSSSLAHPOCKISMSYMHNAVLGGV 279

QY 11 SAIGSVLTSTCERTNGYNTS-SIDLNSVIENVGDS-LKWQPSNFIETC-RNTQLAGSS 68

Db 280 VGTSCSLSPWLMVGLVGLISIGGA 308

QY 69 LAECKTRAQFVSTKINLDDHIANIDGT 97

RESULT 9

ID VATC YEAST STANDARD; PRT; 392 AA.

AC P31412;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE VACUOLAR ATP SYNTHASE SUBUNIT C (EC 3.6.1.34) (V-ATPASE C SUBUNIT)

DE (V-ATPASE 42 KDA SUBUNIT).

GN VMA5 OR VAT3 OR VATC OR YKL080W OR YKL410.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;

OC Saccharomycetaceae; Saccharomyces.

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 99-117.

RX MEDLINE; 92112808.

RA Beltan C., Kopecky J., Pan Y.-C.E., Nelson H., Nelson N.;

RT "Cloning and mutational analysis of the gene encoding subunit C of

RT yeast vacuolar H(+)-ATPase.";

RL J. Biol. Chem. 267:774-779(1992).

RN [2]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE; 93107006.

RA Ho M.N., Hill K.J., Lindorfer M.A., Stevens T.H.;

RT "Isolation of vacuolar membrane H(+)-ATPase-deficient yeast mutants;

RT the VMA5 and VMA4 genes are essential for assembly and activity of

RT the vacuolar H(+)-ATPase.";

RL J. Biol. Chem. 268:221-227(1993).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE; 94262328.

RA James C.M., Gent M.E., Indge K.J., Oliver S.G.;

RT "Sequence analysis of a 10 kb fragment of yeast chromosome XI

RT identifies the SMV1 locus and reveals sequences related to a pre-mRNA

RT splicing factor and vacuolar ATPase subunit C plus a number of

RT unidentified open reading frames.";

RT yeast 10:247-255(1994).

CC -!- FUNCTION: SUBUNIT OF THE PERIPHERAL V1 COMPLEX OF VACUOLAR ATPASE.

CC SUBUNIT C IS NECESSARY FOR THE ASSEMBLY OF THE CATALYTIC SECTOR OF

CC THE ENZYME AND IS LIKELY TO HAVE A SPECIFIC FUNCTION IN ITS

CC CATALYTIC ACTIVITY. V-ATPASE IS RESPONSIBLE FOR ACIDIFYING A

CC VARIETY OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC CELLS.

CC -!- SUBUNIT: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF A

CC PERIPHERAL CATALYTIC V1 COMPLEX (MAIN COMPONENTS: SUBUNIT A, B,

CC C, D, E, AND F) ATTACHED TO AN INTEGRAL MEMBRANE V0 PROTON PORE

CC COMPLEX (MAIN COMPONENT: THE PROTEOLIPID PROTEIN).

CC -!- SIMILARITY: TO V-ATPASE SUBUNIT C FROM OTHER SPECIES.

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CC -----

DR EMBL; M77143; AAA34440.1; -;
DR EMBL; X75560; CAA53237.1; -;
DR EMBL; Z28080; CAA81917.1; -;
DR PIR; S37905; S37905;
DR PIR; S39118; S39118;
DR SGO; L0002460; VNAS;
KW Hydroxylase; Hydrogen ion transport.
FT CONFLICT 1 MATALYTANDFILISLPQNAOPVTA -> MLNLRL (IN
FT REF. 1 AND 2).
SQ SEQUENCE 392 AA; 44188 MW; 0CD1B814046C377E CRC64;

Query Match 12.6%; Score 86; DB 1; Length 392;
Best Local Similarity 24.1%; Pred. No. 2.55e-01;
Matches 21; Conservative 24; Mismatches 36; Indels 6; Gaps 6;

Db 85 ILOGNETSTWARTLPNNMPVPLE-NFQWTRKFKLDSIKDLITLISNESSQLDA 143

Qy 17 VLTSCERTNGYNTSSIDLNSVENVDSLKWQPSNF-IETC-RN-TQL-AG-SSELA 71

Db 144 DVRTATYANYSAKTNLAARKKKTGDL 170

Qy 72 ECKTRAQGFVSTKINLDDHIANIDGTL 98

RESULT 10
ID NANH_CLOSE STANDARD; PRT; 1014 AA.
AC P29767;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE SIALIDASE PRECURSOR (EC 3.2.1.18) (NEURAMINIDASE).
OS Clostridium septicum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
RN [1]
PP SEQUENCE FROM N.A.
RC STRAIN=NC 0054714;
RX MEDLINE; 91238693.
RA Rothe B., Rothe B., Roggentin P., Schauer R.;
RT "The sialidase gene from Clostridium septicum: cloning, sequencing,
RT expression in Escherichia coli and identification of conserved
RT sequences in sialidases and other proteins";
RL Mol. Gen. Genet. 226:190-197(1991).
CC -1- FUNCTION: SIALIDASES HAVE BEEN SUGGESTED TO BE PATHOGENIC FACTORS
CC IN MICROBIAL INFECTIONS.
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF 2,3-, 2,6- AND 2,8-GLYCOSIDIC
CC LINKAGES JOINING TERMINAL NON-REDUCING N- OR O-ACYLNEURAMINYL
CC RESIDUES TO GALACTOSE, N-ACETYLHEXOSAMINE, OR N- OR O-ACETYLED
CC NEURAMINYL RESIDUES IN OLIGOSACCHARIDES, GLYCOPROTEINS,
CC GLYCOLIPIDS OR COLOMINIC ACID.
CC -1- SUBCELLULAR LOCATION: PERIPLASMIC.
CC -1- SIMILARITY: BELONGS TO FAMILY 33 OF GLYCOSYL HYDROLASES.

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CC -----

DR EMBL; X63266; CAA44916.1; -;
DR PIR; S15994; NMCLSS.
DR HSSP; Q02834; 1EUS.
DR PFAM; PF02012; BNR; 4.
KW Hydroxylase; Glycosidase; Periplasmic; Signal; Repeat.

FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 1014 SIALIDASE.
FT REPEAT 431 442 BNR MOTIF.
FT REPEAT 563 574 BNR MOTIF.
FT REPEAT 627 638 BNR MOTIF.
FT REPEAT 700 711 BNR MOTIF.
SQ SEQUENCE 1014 AA; 110652 MW; C4F49233473A2FAD CRC64;

Query Match 12.6%; Score 86; DB 1; Length 1014;
Best Local Similarity 27.1%; Pred. No. 2.55e-01;
Matches 13; Conservative 20; Mismatches 12; Indels 3; Gaps 3;

Db 401 Y-TTKDGTVLASIDVRKGGHDAPN-NIDTGKIRSTDGGVTWDEGKII 446

Qy 9 YNSAIQSGVLTSTCERTNGYNTSSIDLNSVIE-NVDGSLKWPQSFNI 55

RESULT 11
ID AOP2_MOUSE STANDARD; PRT; 223 AA.
AC O08709;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ANTIOXIDANT PROTEIN 2 (EC 1.11.1.7) (NONSELENIUM GLUTATHIONE
DE PEROXIDASE) (1-CYS PEROXIREDOXIN) (1-CYS PRX).
GN AOP2 OR LTW4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
PP SEQUENCE FROM N.A. AND SEQUENCE OF 1-25.
RC STRAIN=DBA/J2, C57BL/6J, AND C3H/FEJ; TISSUE=LIVER, AND KIDNEY;
RX MEDLINE; 97349116.
RA Iakubova O.A., Pacella L.A., Her H., Beier D.R.;
RT "LTW4 protein on mouse chromosome 1 is a member of a family of
RT antioxidant proteins";
RL Genomics 42:474-478(1997).
RN [2]
PP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=SKIN;
RX MEDLINE; 97419117.
RA Munz B., Frank S., Huebner G., Olsen E., Werner S.;
RT "A novel type of glutathione peroxidase: expression and regulation
RT during wound repair";
RL Biochem. J. 326:579-585(1997).
RN [3]
PP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Lee T.H., Yu S.L., Kim S.Y., Kang S.W., Rhee S.G., Seong J.K.,
RA Yu D.Y.;
RT "Characterization of the murine gene encoding 1-Cys peroxidase and
RT identification of highly homologous genes";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: DONOR + H(2)O(2) -> OXIDIZED DONOR + 2 H(2)O.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, KIDNEY AND LIVER.
CC MODERATE EXPRESSION IN BRAIN AND STOMACH. VERY LOW LEVELS IN
CC INTESTINE.
CC -1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY. REHYDRIN SUBFAMILY.

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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; AF004670; AAC53277.1; -;
DR EMBL; Y12883; CAA73383.1; -;
DR EMBL; AF093852; AAC63376.1; -;
DR HSSP; P30041; 1PRX.
DR SWISS-2DPAGE; O08709; MOUSE.
DR MGD; MGI:894320; AOP2.

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KW Oxidoreductase; Peroxidase; Antioxidant; 3D-structure.
FT INIT_MET 0
FT ACT_SITE 47
SQ SEQUENCE 223 AA; 24904 MW; 0B42C96F5CEBEFFC CRC64;

Query Match 12.4%; Score 85; DB 1; Length 223;
Best Local Similarity 30.6%; Pred.No. 3.65e-01;
Matches 15; Conservative 14; Mismatches 18; Indels 2; Gaps 2;

Db 33 GILFSHPDRPTPVC-TTELGRAAKLAPEFAKRNVKLIASIDSVEDHLA 80
QY 45 GSLKWQSPNSFIETCRNTQLAGSSELAECKTRAQQFVSTKIN-LDDHIA 92
| | : | : | | : | : | : | : | : | : | : | : | : | : | : | : |
| | : | : | | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 13
ID ACHEB_RAT STANDARD; PRT; 501 AA.
AC P25109;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE ACETYLCHOLINE RECEPTOR PROTEIN, BETA CHAIN PRECURSOR.
GN CHRN1 OR ACRB.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=MUSCLE;
RX MEDLINE; 9109317.
RA Witzemann V., Stein E., Barg B., Konno T., Koenen M., Kues W.,
RA Criado M., Hofmann M., Sakmann B.;
RT "Primary structure and functional expression of the alpha-, beta-,
RT gamma-, delta- and epsilon-subunits of the acetylcholine receptor
RT from rat muscle.";
RL Eur. J. Biochem. 194:437-448(1990).
CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -1- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
CC DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
CC MUSCLE) CHAINS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC -----
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CC -----
CC EMBL; X74833; CAA52827.1; -.
CC PIR; S13873; SI3873.
CC PFAM; PF00065; neur_chan; 1.
CC PRINTS; PR00252; NRIONCHANNEL.
CC PRINTS; PR00254; NICOTINICR.
CC PROSITE; PS00236; NEUROTROPH_CHANNEL; 1.
CC Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
CC Transmembrane; Phosphorylation.
CC SIGNAL 1 23
CC CHAIN 24 501
CC ACETYLCHOLINE RECEPTOR PROTEIN, BETA
CC CHAIN.
CC DOMAIN 24 244
CC TRANSMEM : 245 269
CC TRANSMEM : 277 295
CC TRANSMEM 311 332
CC TRANSMEM 333 469
CC CYTOPLASMIC (POTENTIAL).
CC DOMAIN 333 469
CC TRANSMEM 470 488
CC TRANSMEM 151 165
CC DISULFID 164 164
CC CARBOHYD 151 165
CC MOD_RES 390 390
CC PHOSPHORYLATION (BY TYR-KINASES)

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FT  PRINTS: PR00254; NICOTINIC.
SQ  SEQUENCE 501 AA; 57026 MW; 2E7DD6AAD1D9364D CRC64;
    Query Match 12.4%; Score 85; DB 1; Length 501;
    Best Local Similarity 29.4%; Pred. No. 3.65e-01;
    Matches 10; Conservative 14; Mismatches 7; Indels 3; Gaps 3;

Db 120 DGNFDVA-LDINVV-SFEGSVRWQPPGLYRSC 151
QY 26 NGGYTSSIDLNSVIENVGSLKQPSN-FIETC 58

RESULT 14
ID ACHB_HUMAN STANDARD; PRT; 501 AA.
AC P11230;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ACETYLCHOLINE RECEPTOR PROTEIN, BETA CHAIN PRECURSOR.
GN CHRNB1 OR CHRNB OR ACHRB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92996503.
RA Beeson D.M.W., Brydson M., Newsom-Davis J.;
RT "Nucleotide sequence of human muscle acetylcholine receptor
RT beta-subunit."
RL Nucleic Acids Res. 17:4391-4391(1989).
RN [2]
RP VARIANT SCCMS MET-285.
RX MEDLINE; 96256490.
RA Gomez C.M., Maselli R., Gammack J., Lasalde J., Tamamizu S.,
RA Cornblath D.R., Lehar M., McNamee M., Kuncel R.W.;
RT "A beta-subunit mutation in the acetylcholine receptor channel gate
RT causes severe slow-channel syndrome."
RL Ann. Neurol. 39:712-723(1996).
RN [3]
RP VARIANT SCCMS MET-289.
RX MEDLINE; 97026281.
RA Engel A.G., Ohno K., Milone M., Wang H.-L., Nakano S., Bouzat C.,
RA Pruitt J.N. II, Hutchinson D.O., Brengman J.M., Bren N., Sieb J.P.,
RA Sine S.M.;
RT "New mutations in acetylcholine receptor subunit genes reveal
RT heterogeneity in the slow-channel congenital myasthenic syndrome."
RL Hum. Mol. Genet. 5:1217-1227(1996).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -!- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
CC DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
CC MUSCLE) CHAINS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- DISEASE: DEFECTS IN ACHRB ARE ONE OF THE CAUSES OF THE SLOW-
CC CHANNEL CONGENITAL MYASTHENIC SYNDROME (SCCMS).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC -----
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CC -----
CC EMBL; X14830; CAA32939.1;
CC PIR; S04607; S04607.
CC MIM; 100710; -.
CC MIM; 601462; -.
CC PFM; PF00065; neur.chan; 1.
CC PRINTS; PR00252; NRIONCHANNEL.

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